

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 07:25:20 : Search time 2.25869 Seconds
(without alignments)
638,431 Million cell updates/sec

Title: US-09-893-615-1
Perfect score: 15
Sequence: 1 WRMYFSHRAHLRSP 15

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: PIR_73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	40.0	296	2 A40996	phenylalanine 4-mo
2	6	40.0	352	2 A71447	hypothetical prote
3	6	40.0	556	2 T19824	hypothetical prote
4	6	40.0	910	2 E88918	2-oxoglutarate deh
5	6	40.0	942	2 C81139	oxoglutarate dehyd
6	6	40.0	943	1 S07776	2-oxoglutarate dehyd
7	6	40.0	943	2 G83448	hypothetical prote
8	6	40.0	1037	2 T27345	hypothetical prote
9	6	40.0	98	2 S39402	hnpf protein - Bra
10	5	33.3	101	2 F72515	hypothetical prote
11	5	33.3	142	2 T22156	hypothetical prote
12	5	33.3	147	2 D83261	probable transcrip
13	5	33.3	148	2 AB0200	conserved hypochet
14	5	33.3	151	2 AC2084	phosphonate metabo
15	5	33.3	176	2 T08254	probable transpos
16	5	33.3	190	2 D70828	hypothetical prote
17	5	33.3	195	2 S34993	hypothetical prote
18	5	33.3	196	2 E83153	nitrite reductase
19	5	33.3	198	2 S25656	conserved hypochet
20	5	33.3	200	2 G83032	T-cell surface gly
21	5	33.3	210	2 T28824	hypothetical prote
22	5	33.3	214	2 AB3589	hypothetical prote
23	5	33.3	216	2 A99323	proteoglycanate 3,
24	5	33.3	216	2 D70554	hypothetical prote
25	5	33.3	216	2 T38520	hypothetical prote
26	5	33.3	217	2 G69547	conserved hypochet
27	5	33.3	225	2 T15228	probable histone B
28	5	33.3	226	2 A11168	transcription regu
29	5	33.3	234	2 A55367	phosphatase cobc -

30	5	33.3	234	2 T34600	hypothetical prote
31	5	33.3	235	1 RWHUT8	T-cell surface gly
32	5	33.3	243	2 C95266	probable ABC trans
33	5	33.3	244	2 T29079	hypothetical prote
34	5	33.3	246	2 T31956	hypothetical prote
35	5	33.3	248	2 B95334	probable transcrip
36	5	33.3	249	2 T37669	hypothetical zinc-
37	5	33.3	252	2 A84866	probable glyoxalas
38	5	33.3	252	2 AC1181	hypothetical prote
39	5	33.3	252	2 AD1538	hypothetical prote
40	5	33.3	253	2 D75301	hypothetical prote
41	5	33.3	254	2 H83334	probable transcrip
42	5	33.3	257	2 T48058	KING-H2 zinc finger
43	5	33.3	261	2 S51935	probable MADS-box
44	5	33.3	270	2 B84813	probable RING zinc
45	5	33.3	273	2 G83968	hypothetical prote

ALIGNMENTS

RESULT 1

A40996 Phenylalanine 4-monooxygenase (EC 1.14.16.1) - Chromobacterium violaceum
M:Alternate names: phenylalaninase; phenylalanine 4-hydroxylase
C:Species: Chromobacterium violaceum
C>Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 31-Mar-2000
C:Accession: A40996; B40996
R:Onishi, A.; Ito, T.; Benkovic, S.J.
J. Biol. Chem. 266, 18454-18459, 1991
A:Title: Cloning and expression of Chromobacterium violaceum phenylalanine hydroxylase
A:Reference number: A40996; MUID:92011593; PMID:1655752
A:Accession: A40996
A:Molecule type: DNA
A:Residues: 1-296 <CONS>
A:Cross-references: GB:M55915; NID:q144481; PID:NAA23115.1; PID:q144482
A:Accession: B40996
A:Molecule type: protein
A:Residues: 1-20 <CONS>
A:Experimental source: strain ATCC 12540
C:Keywords: bioplerin; oxidoreductase

Query Match 40.0%; Score 6; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RHAHLR 13
DB 192 RHAHLR 197

RESULT 2

A71447 hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: Columbia
C>Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
C:Accession: A71447
P:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Medler, H.; Medler, E.; Mambut, R.; Woltzenegger, I.; Pohl, T.M.; Terry, N.; Avramopoulos, T.; Hempel, S.; Kotter, P.; Ertan, K.D.; Riegler, M.; Schaeffer, M.; Funk, Nature 391, 485-486, 1998
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Monfort, A.; Pons, A.; Puigdomenech, A.; Moore, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; C.; Chalvatiz, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis
A:Reference number: A71400; MUID:9812113; PMID:9461215
A:Accession: A71447
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-352 <BEV>
C:Cross-references: GB:297344; NID:92245126; PID:e33707H; PID:92245129
C:Genetics:

A:Map position: 4COP9-4G3845

Query Match 40.0%; Score 6; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 ARLRSP 15
111111
DB 179 ARLRSP 184

RESULT 3

T19824
hypothetical protein C38D4.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

Accession: T19824

Notes: L. submitted to the EMBL Data Library, October 1994

A:Reference number: Z19183

A:Accession: T19824

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-556 <MULT>

A:Cross-references: EMBL:246241; PIDN:CAA86317.1; GSPDB:GN00021; CESP:C38D4.4

A:Experimental source: clone C38D4

C:Genetics:

A:Gene: CESP:C38D4.4

A:Map position: 3

A:Insertions: 40/2; 80/2; 148/3; 257/3; 370/1; 405/1; 488/3

Query Match 40.0%; Score 6; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 ARLRSP 15
111111
DB 126 ARLRSP 131

RESULT 4

E89918

2-oxoglutarate dehydrogenase E1 [imported] - *Staphylococcus aureus* (strain N315)

C:Species: *Staphylococcus aureus*

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

Accession: E89918

Notes: M. Ohta, T. Uchiyama, I. Baba, T. Yuzawa, H. Kobayashi, I. Cui, L. Oguc

ma, A. Mizutani-Oi, Y. Kobayashi, N. Sawano, T. Inoue, R. Kaito, C. Sekimizu, K. C. Shiba, T. Hattori, M. Ogasawara, N. Hayashi, H. Hiratsuka, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: E89918

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-910 <KOR>

A:Cross-references: GB:BA000018; PID:q13701210; PIDN:BA842505.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: odhA

C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding dom

Query Match 40.0%; Score 6; DB 2; Length 910;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10
111111
DB 599 FSHRHA 604

RESULT 5

E89918

probable oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) E1 component NMA1149 [3

C:Species: *Neisseria meningitidis*

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001

Accession: C01139; H81881

Notes: R. Rettelin, H. Saunders, N.J. Heidelberg, J. Jeffries, A.C. Nelson, K.E. Eisen,

Hickey, E.K.; Hatt, D.H.; Salberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B

li, H.; Qin, H.; Yamachavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.

Science 287, 1809-1815, 2000

A:Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.

A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: C01139

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-942 <TEF>

A:Cross-references: GB:AE002446; GB:AE002098; NID:q7226135; PIDN:AAE41361.1; PID:q72

A:Experimental source: serogroup B, strain MC58

R. Parthill, J. Achtman, M. James, K.D. Bentley, S.D. Churcher, C. Klee, S.R. McK

night, S.; Jorgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajand

ature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2493

A:Reference number: A81775; MUID:2022556; PMID:10761919

A:Accession: H81881

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-942 <PAR>

A:Cross-references: GB:AL162755; GB:AL157959; NID:q7379742; PIDN:CAE84411.1; PID:q737

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: suca; MMB0955; NMA1149

C:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding

C:Keywords: oxidoreductase

Query Match 40.0%; Score 6; DB 2; Length 942;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10
111111
DB 626 FSHRHA 631

RESULT 6

S07776

oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) - *Azotobacter vinelandii*

N:Alternative names: 2-oxoglutarate dehydrogenase complex chain E1

C:Species: *Azotobacter vinelandii*

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Oct-1999

Accession: S07776

Notes: R. Schilke, E. Westphal, A.H.; Hanemaaijer, R.; de Kok, A.

Eur. J. Biochem. 187, 229-234, 1990

A:Title: The 2-oxoglutarate dehydrogenase complex from *Azotobacter vinelandii*. I. Mol

A:Reference number: S07776; MUID:9016823; PMID:2404759

A:Accession: S07776

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-943 <SCCH>

A:Cross-references: GB:X52433; NID:q39231; PIDN:CAA36680.1; PID:q39232

C:Genetics:

A:Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding

C:Keywords: oxidoreductase; thiamin pyrophosphate; tricarboxylic acid cycle

E:359-405/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 40.0%; Score 6; DB 1; Length 943;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10
111111
DB 631 FSHRHA 636

RESULT 7

G83448

2-oxoglutarate dehydrogenase (el subunit) PA1585 [imported] - Pseudomonas aeruginosa (strain ATCC 27801)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: G83448

R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Badman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,

; Lox, S.; Olson, M.V.

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: G83448

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-943 <STO>

A:Cross-references: GB:AE004586; GB:AE004091; NID:g9947536; PIDN:ACG04974.1; GSPDB:GN001

C:Genetics:

A:Gene: sucA, PA1585

C:Superfamily: Oxoglutarate dehydrogenase (lipoamide): thiamin pyrophosphate-binding domain

Query Match

Best Local Similarity 40.0%; Score 6; DB 2; Length 943;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FSHRHA 10

DB 631 FSHRHA 636

RESULT 8

T27345

hypothetical protein Y70C5A.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27345

R:Steward, C.

A:Title: The EMBL Data Library, September 1997

A:Reference number: Z20349

A:Accession: T27345

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1037 <WIL>

A:Cross-references: EMBL:Z59282; PIDN:CAB16532.1; CESP:Y70C5A.2

C:Genetics:

A:Gene: CESP:Y70C5A.2

A:Intons: 21/2; 71/1; 144/3; 246/1; 283/1; 319/2; 559/3; 636/3; 671/2; 950/3

Query Match

Best Local Similarity 40.0%; Score 6; DB 2; Length 1037;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHRSP 15

DB 983 AHRSP 988

RESULT 9

S39402

hupf protein - Bradyrhizobium japonicum

C:Species: Bradyrhizobium japonicum

C:Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 24-Sep-1999

C:Accession: S39402

R:Van Soest, C.; Brown, J.; Verreth, C.; Vanderleyden, J.

J. Mol. Biol. 234, 508-512, 1993

A:Title: Nucleotide sequence analysis of four genes, hupC, hupD, hupE and hupG, C.ustr

A:Reference number: S39400; MUID:94047099; PMID:8230232

A:Accession: S39402

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-98 <VAN>

A:Cross-references: EMBL:Z21948; NID:g311536; PIDN:CA77545.1; PID:g311539

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 199

C:Superfamily: hydroxylase expression/formation protein hupC

Query Match

Best Local Similarity 33.3%; Score 5; DB 2; Length 98;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHRSP 14

DB 93 AHRSP 97

RESULT 10

F72515

hypothetical protein APE2099 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: F72515

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Takawa, Y.; Jin-no, K.

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, Y.; Yamazaki

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Cremonarchaeon, /

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: F72515

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-101 <KAW>

A:Cross-references: DBJ:AP000063; NID:g5105654; PIDN:BA81110.1; PID:g5105798

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE2099

C:Superfamily: Aeropyrum pernix hypothetical protein APE2099

Query Match

Best Local Similarity 33.3%; Score 5; DB 2; Length 101;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 AHRSP 14

DB 2 AHRSP 6

RESULT 11

T22156

hypothetical protein F44A6.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T22156

R:Sulston, J.

A:Title: The EMBL Data Library, August 1995

A:Reference number: Z19524

A:Accession: T22156

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-142 <WIL>

A:Cross-references: EMBL:Z50858; PIDN:CAA90724.1; GSPDB:GN00028; CESP:F44A6.4

A:Experimental source: clone F44A6

C:Genetics:

A:Gene: CESP:F44A6.4

A:Map position: X

A:Superfamily: Caenorhabditis elegans hypothetical protein F44A6.4

Query Match

Best Local Similarity 33.3%; Score 5; DB 2; Length 142;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 HRHAH 11

DB 4 HRHAH 8